
Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Jun 08 19:36:04 EDT 2007

Validated By CRFValidator v 1.0.2

Application No: 10661742 Version No: 1.1

Input Set:

Output Set:

Started: 2007-06-08 19:35:50.118

Finished: 2007-06-08 19:35:56.264

Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 146 ms

Total Warnings: 15

Total Errors: 26

No. of SeqIDs Defined: 19

Actual SeqID Count: 19

| Error code | | Error Description |
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| W | 213 | Artificial or Unknown found in <213> in SEQ ID (1) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (2) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (5) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (6) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (7) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (8) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (9) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (10) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (11) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (16) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (17) |
| E | 257 | Invalid sequence data feature in <221> in SEQ ID (17) |
| E | 257 | Invalid sequence data feature in <221> in SEQ ID (17) |
| E | 257 | Invalid sequence data feature in <221> in SEQ ID (17) |
| E | 257 | Invalid sequence data feature in <221> in SEQ ID (17) |
| E | 257 | Invalid sequence data feature in <221> in SEQ ID (17) |
| E | 257 | Invalid sequence data feature in <221> in SEQ ID (17) |
| E | 257 | Invalid sequence data feature in <221> in SEQ ID (17) |

Input Set:

Output Set:

Started: 2007-06-08 19:35:50.118 **Finished:** 2007-06-08 19:35:56.264

Elapsed: 0 hr(s) 0 min(s) 6 sec(s) 146 ms

Total Warnings: 15
Total Errors: 26
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Actual SeqID Count: 19

| Error code | | Error Description | | | | | | | | | | |
|------------|-----|--|--|--|--|--|--|--|--|--|--|--|
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| W | 213 | Artificial or Unknown found in <213> in SEQ ID (19) | | | | | | | | | | |
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| E | 257 | Invalid sequence data feature in <221> in SEQ ID (19) | | | | | | | | | | |
| E | 257 | Invalid sequence data feature in <221> in SEQ ID (19) This error has occured more than 20 times, will not be displayed | | | | | | | | | | |

SEQUENCE LISTING

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<151> 2001-03-15
<160> 19
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Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
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                            40
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                        55
Asn Thr Thr Gly Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
                                    90
Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
Tyr Leu Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
                                               125
      115
                          120
Thr Ser Val Glu Ser Val Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
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135

140

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Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys 180 \$185\$

Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys

195 200 205

Ser Ile Gln Met Met Arg Gln Tyr Thr Ser Phe His Phe Ala Ser Leu 210 215 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp 225 230 235 240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys 245 250 255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu 260 265 270

Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys 275 280 285

Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met 290 295 300

Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser 305 310 315 320

His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
325 330 335

Thr Glu Glu Gly Val Glu Ala Ala Ala Thr Ala Val Val Val Val 340 345 350

Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro 355 360 365

Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr 370 375 380

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

construct

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gttcatcacc agtttcaaaa gcttctgact gaattcaaca aattccactg atgcatatga 300
gctgaagatc gccaacaagc tcttcggaga aaaaacgtat ctatttttac aggaatattt 360
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ctatttcaaa gggcagtggg agaagaaatt taataaagaa gatactaaag aggaaaaatt 600
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                                                                  1193
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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
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<400> 4
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<211> 20
<212> DNA
<213> Artificial Sequence
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| <223> | Description of Artificial primer | Sequence: | Synthetic |
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| .0.7.0 | | | |
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| 1210, | merriciar bequence | | |
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| | primer | | |
| | | | |
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| <212> | | | |
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| <223> | Description of Artificial | Sequence: | Synthetic |
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| | | | |
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| <220> | Doggription of Antificial | Comionas | Synthotic |
| <2Z3> | Description of Artificial primer | sequence: | Synthetic |
| | bilmer | | |
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| attag | ttgaa ggagatgata attc | | 24 |
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| <211> | | | |
| <212> | | | |
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| | primer | | |
| | primer | | |

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      construct
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gatgccatca agaaatttta ccagaccagt gtggaatctg ttgattttgc aaatgctcca 420
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gtcctcttag gagccaaaga caacactgca caacagatta agaaggttct tcactttgat 180
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caagtcacag agaacaccac aggaaaagct gcaacatatc atgttgatag gtcaggaaat 240

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| Thr | Ala 50 | Gln | Gln | Ile | Lys | Lys 55 | Val | Leu | His | Phe | Asp 60 | Gln | Val | Thr | Glu |
| Asn 65 | Thr | Thr | Gly | Lys | Ala 70 | Ala | Thr | Tyr | His | Val 75 | Asp | Arg | Ser | Gly | Asn 80 |
| Val | His | His | Gln | Phe 85 | Gln | Lys | Leu | Leu | Thr 90 | Glu | Phe | Asn | Lys | Ser 95 | Thr |
| Asp | Ala | Tyr | Glu 100 | Leu | Lys | Ile | Ala | Asn 105 | Lys | Leu | Phe | Gly | Glu 110 | Lys | Thr |
| Tyr | Leu | Phe 115 | Leu | Gln | Glu | Tyr | Leu 120 | Asp | Ala | Ile | Lys | Lys 125 | Phe | Tyr | Gln |
| Thr | Ser 130 | Val | Glu | Ser | Val | Asp 135 | Phe | Ala | Asn | Ala | Pro 140 | Glu | Glu | Ser | Arg |
| Lys 145 | Lys | Ile | Asn | Ser | Trp 150 | Val | Glu | Ser | Gln | Thr 155 | Asn | Glu | Lys | Ile | Lys 160 |
| Asn | Leu | Ile | Pro | Glu 165 | Gly | Asn | Ile | Gly | Ser 170 | Asn | Thr | Thr | Leu | Val 175 | Leu |
| Val | Asn | Ala | Ile 180 | Tyr | Phe | Lys | Gly | Gln 185 | Trp | Glu | Lys | Lys | Phe 190 | Asn | Lys |
| Glu | Asp | Thr 195 | Lys | Glu | Glu | Lys | Phe 200 | Trp | Pro | Asn | Lys | Asn 205 | Thr | Tyr | Lys |
| Ser | Ile 210 | Gln | Met | Met | _ | Gln 215 | _ | Thr | Ser | Phe | His 220 | Phe | Ala | Ser | Leu |
| Glu 225 | Asp | Val | Gln | Ala | Lys 230 | Val | Leu | Glu | Ile | Pro 235 | Tyr | Lys | Gly | Lys | Asp 240 |
| Leu | Ser | Met | Ile | Val 245 | Leu | Leu | Pro | Asn | Glu 250 | Ile | Asp | Gly | Leu | Gln 255 | Lys |
| Leu | Glu | Glu | Lys 260 | Leu | Thr | Ala | Glu | Lys 265 | Leu | Met | Glu | Trp | Thr 270 | Ser | Leu |
| Gln | Asn | Met 275 | Arg | Glu | Thr | Arg | Val 280 | Asp | Leu | His | Leu | Pro 285 | Arg | Phe | Lys |
| Val | Glu 290 | Glu | Ser | Tyr | Asp | Leu 295 | Lys | Asp | Thr | Leu | Arg 300 | Thr | Met | Gly | Met |
| Val 305 | Asp | Ile | Phe | Asn | Gly 310 | Asp | Ala | Asp | Leu | Ser 315 | Gly | Met | Thr | Gly | Ser 320 |
| Arg | Gly | Leu | Val | Leu | Ser | Gly | Val | Leu | His | Lys | Ala | Phe | Val | Glu | Val |

Thr Glu Glu Gly Ala Glu Ala Ala Ala Thr Ala Val Val Gly Phe 345 Gly Ser Ser Pro Ala Ser Thr Asn Glu Glu Phe His Cys Asn His Pro 365 355 360 Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr 375 Gly Arg Phe Ser Ser Pro 385 390 <210> 15 <211> 390 <212> PRT <213> Homo sapiens <400> 15 Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe 10 Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile 25 Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn 35 40 Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu 50 55 Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn 70 75 65 Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr 85 90 Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr 105 Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln 120 115 Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg 130 135 140 Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys

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Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Asn Lys Phe Lys Lys

185

155

170

160

150

165

180

195 200 205

Ser Val Gln Met Met Arg Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu 210 215 220

Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp 225 230 235 240

Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys 245 250 255

Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu 260 265 270

Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys